```
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89921
A;Status: preliminary
A;Retus: preliminary
A;Residues: 1.3890 «KUR»
A;Residues: 1.3890 «KUR»
A;Residues: UNIPROT:099U53; GB:BA000018; PID:g13701233; PIDN:BAB42528.1; GSPDB:CCGGenetics:
C;Genetics:
A;Gene: ebhB
                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                         60 TPINGTNSLTKKVPGLKKDGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDGPRIEL 119
                                                                                                                                                                                                                                                                                                                                                   120 EAAYQQ---FNPKNTDN-NDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 CYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPBVSAFIGGYHG 235
                                                                                                                                                                                                                                                                               3 YKKILVRSALISLMSILPYQ---SFADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEE 59
                                                                                                                                                                                 Query Match 6.7%; Score 98; DB 2; Length 3890;
Best Local Similarity 22.3%; Pred. No. 49;
Matches 65; Conservative 48; Mismatches 114; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 VIGNKFEKIPVIT--PVVLND-----APQTTSASVTLDVGYFGGEIGMRFT 279
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Search completed: February 17, 2005, 16:58:05 Job time : 42 secs

us-10-680-349-42.rpr

| A;Molecule type: mRNA A;Rosidues: 1-69 <sit> A;Cross-references: GB:M62972; NID:g157263; PIDN:AAA28476.1; PID:g157267 A;Experimental source: embryo</sit> | 156QOYVULKNDGITFMSLMVNTCYDITAEGVSFVPYACAGIGADLITIFKD |
|--|---|
| A;Gene: DmkP140 A;Cross-references: FlyBase:FBgn0003276 A;Introns: 8/1 | QY 205 INLKRAYQGKIGISYPITPRVSAFIGGYYHQVIGNKFEKIPV1TPV 250 |
| C;Superfamily: DNA-directed RNA polymerase 132K polypeptide C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger | 251VLNDAPQTTSASVTLD-VGYFGGE 273 |
| Query Match Best Local Similarity 19.9%; Pred. No. 4.7; Matches 53; Conservative 39; Mismatches 78; Indels 96; Gaps 12; | |
| 21 YQSFADFVGSRTNDNKEGFYISAKYNPSISHFRKFS | |
| Qy 81 ITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDGPRIELEAAYQQFNPKNTDNNDTDNGE 140 | C. Donners L. Tron-2014 #Bequence_revision 2/-NOV-2001 #Lext_Change 03-011-2004 C. Accession: AC1153 R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. |
| Qy 141 YYKHRALSRKDAMEDQQYVVLKNDGITFMSLMVNTCY 177 : | D.; Jones, L.M.; Karst, U. Science 294, 84-852, 2001 Science 294, 849-852, 2001 Althore: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, |
| Qy 178 DITAEGVSFVPYACAGIGADLITIPKDLNLKF-AYQGKIGISY 219 | A;Title: Comparative genomics of Listeria species. A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Accession: AC1153 A;Status: preliminary |
| Qy 220 PITPEVSAFIGGYYHGVIGNK 240 :: : : : Db 1003 PFNDAVNVQKISTFLQEYGYHLRGNE 1028 | A;Molecule type: DNA_ A;Residues: 1-1582 <gla> A;Cross-references: UNIRROT:08Y9A5; GB:NC_003210; PIDN:CAC98705.1; PID:g16410016; GSPDB:C A;Experimental source: strain EGD-e C;Genetics:</gla> |
| RESULT 13 B70448 3-oxoscyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Aquifex aeolicus C.Speries: Amifex aeolicus | Query Match Best Local Similarity 21.4%; Pred. No. 10; Marches 63: Conservative 30: Mismatches 84: Indels 118: Gaos 13: |
| C.Date: 08-May-1998 #Bequence_revision 08-May-1998 #text_change 09-Jul-2004 C.Accession: B70448 R.Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov | 39 FYISAKYNPSISHFRKFSAEETPINGTNSLTKKVFGLKKDGDITKKDDFTRVAPGIDFQN 98 |
| Vature 392, 353-358, 1998 A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A,Reference number: A70300; MUID:98196666; PMID:9537320 | 99 NLISGESGSIGYSMDGPRIELERAAYQQFNPKNTDNNDTDNGE |
| A;Accession: B70448 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA A;Bolecule type: DNA A;Rolecule type: DNA | Db 584 DLISNVDGSTIKPIDGFQKEKPHVVKENAKSTATLQDEDDFDFDYVTFIKTFEVIPSEGK 543 Qy 141 YYKHPALSRKDAMEDQQYVVLKNDGITFWSLMVN 174 .: |
| A/NCOSB-LUCE: 1-113 NALY A/Experimental Bource: UNIPROT:067612; GB:AE000752; NID:g2984021; PIDN:AAC07574.1; PID:g298 C/Genetics: | Db 644 VFEKTRLSADÅBEKTARNMIGNDIMGSALKDYTPLADDGRITSPRÍYMYZEMNINPSGVB 703 Qy 175TCYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPEVSAFI 229 |
| A)Gene: fabF C)Function: a)Darbhav. fartv acid bicavmthesis | Db 704 DTLNSSFIDTLPRGLKMLBYDIAGLNSS731 |
| Affactivey: Lacty acts Diopyliments Synthase I; 3-oxoacyl-[acyl-carrier-prot C;Superfailly: 3-oxoacyl-[acyl-carrier-prot C;Superfailly: 3-oxoacyl-[acyl-carrier-prot C;Keywords: acyltransferase; fatty acid biosynthesis F;23-410/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <oas> F;165/Active site: Cys #status predicted</oas> | QY 230 GGYYHGVIGNKFEKIPVITPVVLNDAPQTTSASVTL-DVGYFG 271 : : |
| Query Match 6.9%; Score 101.5; DB 2; Length 415; Best Local Similarity 21.7%; Pred. No. 1.3; Matches 60; Conservative 32; Mismatches 73; Indels 111; Gaps 14; | RESULT 15 C89921 Pypothetical protein ebhB [imported] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus |
| OY 62 INGTNSLTKKVFGLKKDGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDGPR 116 | C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: C89921 R;Kuroda, M.; Ohta, T.; Uchlyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguct |
| QY 117 IELEAAYQQFNPKN-TDNNDTDNGEYYKHPALSR-KDAMED | ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, K.; F. C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hixamatsu, K. Lancet 357, 1225-1240, 2001 A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. |

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

- protein search, using sw model OM protein

Run on:

February 17, 2005, 16:48:20

; Search time 40 Seconds (without alignments) 673.517 Million cell updates/sec

US-10-680-349-42

1 MNYKKILVRSALISLMSILP.....ASVTLDVGYFGGEIGMRFTF 280 score: Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | surface | surface | surface | 28k surface antige | major antigenic pr | 28k surface antige | major surface prot | 28k surface antige | heat resistant agg | probable outer mem | hemolysin A precur | DNA-directed RNA p | 3-oxoacyl-[acyl-ca | adhesin homolog lm | hypothetical prote | heat resistant agg | DNA-directed RNA p | glutamate rich pro | glycosidase homolo | outer cell wall pr | peptidoglycan boun | 6-Phospho-Beta-D-G | endo-beta-N-acetyl | hypothetical prote | | hypothetical prote | conserved hypothet | hypothetical prote | prophage pi2 prote |
|-----------|---------------|---------|---------|---------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΙD | | | JE0217 | JE0216 | 140882 | | | - | 154668 | | | A27826 | B70448 | AC1153 | C89921 | AC3295 | | | | | • | | | F71639 | H64473 | T51370 | | C974 | F86754 |
| | 8 | | | | N | | | | | ~ | | | | N | ~ | ~ | ~ | | | N | | | | | | | 7 | | | - |
| | Length | 276 | 286 | 280 | 278 | 284 | 287 | 282 | 133 | 264 | 239 | 738 | 1176 | 415 | 1582 | 3890 | 274 | 1174 | 1271 | 1310 | 1004 | 1578 | 474 | 658 | 180 | 608 | 745 | 219 | 219 | 401 |
| عد | Query | 43.1 | 42.4 | 41.2 | 39.9 | 38.6 | 35.3 | 26.4 | 15.6 | 8.2 | 7.4 | 7.1 | 7.0 | 6.9 | 6.8 | 6.7 | 6.7 | 6.7 | 6.7 | • | 6.5 | ٠ | 6.5 | 6.4 | 6.4 | 6.4 | 6.4 | • | 6.3 | 6.3 |
| | Score | N | 620 | 603 | 583 | 565 | 515.5 | 386.5 | 227.5 | 119.5 | 107.5 | 104.5 | 102 | 101.5 | 100 | 98 | 97.5 | 97.5 | 97.5 | 97.5 | 95 | 95 | 94.5 | 93.5 | 93 | 93 | 93 | N | 92.5 | N |
| | Result No. | | 7 | m | 4 | ស | 9 | 7 | æ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 11 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | | 28 | 29 |

| probable electron | endo-beta-N-acetyl | DNA-directed RNA p | hemolysin [importe | opacity protein op | penicillin-binding | TyB protein - yeas |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| C69336 | C97980 | A25884 | AI0452 | S16617 | AG0517 | B23496 | 869967 | 869953 | S58651 | S70233 | 996698 | 869950 | 870230 | S53592 | 869973 |
| ~ | ~ | N | ~ | ~ | N | N | N | ~ | N | N | N | N | N | ~ | 7 |
| 585 | 721 | 1224 | 1635 | 282 | 588 | 1348 | 1598 | 1770 | 1770 | 1770 | 1770 | 1770 | 1770 | 1771 | 1810 |
| 6.3 | 6.3 | 6.3 | 6.3 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 | 6.2 |
| 92.5 | 91.5 | 91.5 | 91.5 | 91 | 91 | 16 | 91 | 91 | 91 | 91 | 91 | 91 | 91 | 91 | 91 |
| 30 | 31 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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| | | antigen |
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| SG | 02 | × |

28k surface antigen 5 - Bhrlichia chaffensis
NiAlternate names: MAP1
(Species: Ehrlichia chaffensis
CiSpecies: Ehrlichia chaffensis
CiSpecies: Ehrlichia chaffensis
CiSpecies: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
CiAccession: JE0218
CiBace: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
CiAccession: JE0218
CiBace: Commun. 247, 636-643, 1998
CiBace: Diophys. Res. Commun. 247, 636-643, 1998
Cifference number: JE0216; MUID:98321180; PMID:9647746
Cibacession: JE0218
Cibacess

Gaps Query Match 43.1%; Score 629.5; DB 2; Length 276; Best Local Similarity 47.9%; Pred. No. 8.3e-44; Matches 137; Conservative 41; Mismatches 87; Indels 21;

9

99 1 MNYKKVFITSALISLISSLPGVSFSDPAGSGINGN---FYISGKYMPSASHFGVFSAKE-1 MNYKKILVRSALISLMSILPYQSPADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEET ⋧

61 PINGTNSLTKKVFGLKKDGD-----ITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDG 114 셤 ò

57

g

115 PRIELEAAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMB----DQQYVVLKNDGITFMS 170 ઠે

g

171 IMVNTCYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPEVSAFIG 230 ద ò

231 GYYHGVIGNKFEKIPVITPVVLNDAPQ-TTSASVTLDVGYFGGEIG 275 |::| ||||:| || || || || GSTLAGKGNYPAIVILDVCHFGIEMG 276 231 셤 ò

28k surface antigen 2 - Ehrlichia chaffensis
NyAlternate names: MAP1
NyAlternate names: MAP1
Species: Brilichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0219
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28Abs surface antigen gene family of the tribe i A;Reference number: JE0216; MUID:98321180; PMID:9647746

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28
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20k surface antigen 4 - Ehrlichia chaffensis
20k surface antigen 4 - Ehrlichia chaffensis
20k surface antigen 5 - Ehrlichia chaffensis
C; Accession: Ehrlichia chaffensis
C; Accession: MC217
R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A; Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe
A; Reference number: JE0216; MUID:98321180; PMID:9647746
A; Accession: JE0217
A; Molecule type: DNA
A; Residues: 1-280 cRED>
A; Cross-references: UNIPROT:052107; GB:AF062761
                                                                                                                                                                                                                         60 TPINGTNSLTKKVFGLKKDGD-----ITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMD 113
                                                                                                                                                                                                                                                                 GPRIBLEAAYQQFNPRWTDNNDTDNGEYYKHFALSRKDAMEDQ-----QYVVLKNDGIT 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GPRIELEMSYETFDVKNOGNNYKNDA--HKYYALTHNSGGKLSNAGDKFVFLKNEGLLDI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLMVNTCYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPEVSAFI 229
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                                                                          42.4%; Score 620; DB 2; Length 286; 47.3%; Pred. No. 5.2e-43; Live 42; Mismatches 89; Indel8
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            A;Molecule type: DNA
A;Residues: 1-286 <RED>
A;Cross-references: UNIPROT:052105; GB:AF062761
                                                                                          Best Local Similarity 47.3:
Matches 139; Conservative
A; Accession: JE0219
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A;Residues: 1-284 <RES>
A;Cross-references: UNIPROT:Q46327; EMBL:X74250; NID:g454266; PIDN:CAA52309.1; PID:g45420
28k surface antigen 3 - Ehrlichia chaffensis
NyAlternate names: MAP1
C;Species: Bhrlichia chaffensis
C;Species: Bhrlichia chaffensis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE0216
C;Accession: JE0216
C;A. Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 284bas surface antigen gene family of the tribe A;Reference number: JE0216, MUID:98321180; PMID:9647746
A;Reference number: JE0216
A;Reference n
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Cispecies: Cowdria ruminantium (heartwater rickettsia)
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Cispecies: Cowdria ruminantium (heartwater rickettsia)
Cispecession: I40882; 842827
Rivan Vliet, A.H.; Jongejan, F.; van Kleef, M.; van der Zeijst, B.A.
Infect. Immun. 62, 1451-1456; 1994
Airtle: Molecular cloning, sequence analysis, and expression of the gene encoding the Airtle: Molecular cloning, sequence analysis, and expression of the gene encoding the Airtle: Molecular cloning, sequence analysis, and expression of the gene encoding the Airtle: Molecular cloning, remained from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 TPINGTNSLTKKVFGLKKD-----GDITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----EKNPTVALYGLKQDWEGISSSSHNDNHFNNKGYSFKYENNPFLGFAGAIGYSMGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 PRIELEAAYQQFNPKNTDNNDTDNGEYYKHFALSRKD---AMEDQQYVVLKNDGITFMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 MVNTCYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPEVSAFIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 KMSIKEDSRD----TKAVFGLKKDWDGVKTPSGNTNSIFTEKDYSFKYENNPFLGFAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 IGYSMDGPRIELEAAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGIŢ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 278;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
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38.6%; Score 565; DB 2;
Best Local Similarity 43.1%; Pred. No. 1.5e-38;
Matches 129; Conservative 39; Mismatches 97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.9%; Score 583; DB 2;
ilarity 43.6%; Pred. No. 5.1e-40;
Conservative 49; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 126; Conserv
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28k surface antigen 2 - Ehrlichia canis
C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
C;Accession: JE021
R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Biochem. Biophya: Res. Commun. 27, 636-643, 1998
A;Title: Molecular characterization of a 28kbs surface antigen gene family of the tribe I
A;Reference number: JE0216; MUID:98321180; PMID:9647746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MOlecule type: DNA
A;Residues: 1-133 <RED>
A;Cross-references: UNIPROT:085360; GB:AF062762; NID:g3327964; PIDN:AAC26722.1; PID:g3327
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Cispecies: Escherichia coli
Cipate: O'Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
CiAccession: 154668; 169133; 169134
R;Lutwyche, P.; Rupps, R.; Cavanagh, J.; Warren, R.A.; Brooks, D.E.
A;Fict: Immun. 62, 5020-5026, 1994
A;Title: Cloning, sequencing, and viscometric adhesion analysis of heat-resistant agglut:
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A;Accession: 169133
   ė,
                                                                                                                                                                                                                               163 NDGITFMSLMVNTCYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPIT 222
                                                                                                                                                                                                                                                                                                                                                              ----EKKKKTTVVYGLKENWAGDAISSOSPDDNFTIRNYSFKYASNKFLGFAVAIGYSIGS 113
                                                                                                                                                                                          50 SHF--RKFSAEETPINGTNSLTKKVFGLKKDGDITKKDDFTRVAPGIDFQNNLISGFSGS 107
                                                                                                                                                                                                                                                                                                                      108 IGYSMDGPRIBLEAAYQQFNPKNTDNNDTDNGEYYKH-----FALSRKDAMEDQQYVVLK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PINGTNSLTKKVFGLKKD--GDI----TKKDDFTRVAPGIDFQNNLISGFSGSIGYSMDG 114
                                                                                                       1 MNYKKILVRSALISLMSILPYQSFADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEET 60
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      Gapa
      35;
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   Mismatches 113; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.6%; Score 227.5; DB 2
41.4%; Pred. No. 1.6e-11;
iive 20; Mismatches 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A,Molecule type: DNA
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      54;
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Best Local Similarity 41.4%;
Matches 58; Conservative
   Conservative
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196
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   Matches
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Cipecies: Ehrlichia canis

Cipate: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

Cipate: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

Cipate: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

Cipate: 21-Aug-1998 #sequence_revision 247, 636-643, 1998

Biochem. Biophys. Res. Commun. 247, 636-643, 1998

A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe

A;Accession: JB0220

A;Accession: JB0220

A;Molecule type: DNA

A;Residues: 1-287 <RED>

A;Cross-references: UNIPROT:Q9ZGJ0; GB:AF062762; NID:g3327964; PIDN:AAC26721.1; PID:g332
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C;Genetics:
A;Gene: msp4
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C; Species: Anaplasma marginale
C; Species: Anaplasma marginale
C; Species: 19-011-1996 #sequence_revision 19-011-1996 #text_change 09-01-2004
C; Date: 136, 291-294, 1993
R; Oberle, S. M.; Barbet, A.F.
Gene 136, 291-294, 1993
A; Title: Derivation of the complete msp4 gene sequence of Anaplasma marginale without A; Reference number: 139648; MUID:94124017; PMID:8294020
A; Accession: 139648
A; Reference number: Tanslated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-282 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----BQSFTKVLVGLDQRLSHNIINNNDTAKSLKVQNYSFKYKNNPFLGFAGAIGYSIGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | | | | | ::: |: | | | | | | | | srielsus Shira Calsher Cals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- DTDNGEYYKHFALSRKDAMED 155
FMSLMVNTCYDITAEGVSFVPYACAGIGADLITIFKDLNLKFAYQGKIGISYPITPEVSA 227
                                 168 DISLMLNACYDIMLDGMPVSPYVCAGIGTDLVSVINATNPKLSYOGKLGISYSINPEASI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                            1 MNYKKILVRSALISLMSILPYQSFADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEET
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                                                                                                                        PIGGYYHGVIGNKFEKIPVITPVVLNDAPQTTS-----ASVTLDVGYFGGEIGMRFTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 386.5; DB 2; Length 282; Pred. No. 5.1e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 515.5; DB 2; Length 2; Pred. No. 1.7e-34; 47; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                               JE0220
28k surface antigen 1 - Ehrlichia canis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.3%;
Best Local Similarity 39.3%;
Matches 120; Conservative 4
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Best Local Similarity
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C. Accession: S01892
R.Alm, R.A.; Stroeher, U.H.; Manning, P.A.
Mol. Microbiol. 2, 481-488, 1988
A. Title: Extracellular proteins of Vibrio cholerae: nucleotide sequence of the structural in the non-heamolytic classical strain 5698.
A.Reference number: S01892; MUID:89013889; PMID:3050359
A.Molecule type: DNA
A.Residues: 1-738
A.Molecule type: DNA
A.Residues: 1-738
A.Molecule type: Company of the structural classical strain solutions of the structural strain stra
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C,Species: Drosophila melanogaster
C,Species: Drosophila melanogaster
C,Species: Drosophila melanogaster
C,Species: Drosophila
R,Falkenburg, D.; Dworniczak, B.; Faust, D.M.; Bautz, E.K.F.
J, Mol. Biol. 195, 929-337, 1987
A,Title: RNA polymerase II of Drosophila. Relation of its 140,000 Mr subunit to the beta A,Reference number: A27826
A,Arcession: A27826
A,Arcession: A27826
A,Molecule type: DNA
A,Residues: 54-1176 <RAL>
A,Cross-references: UNIPORT.P08266; GB:X05709; GB:M29646; NID:G5514651; PIDN:CAA29180.2;
A,Molecule type: DNA
A,Residues: S, Oldenburg, I.; Petersen, G.; Bautz, E.K.F.
Gene 100, 155-162, 1991
A,Title: Analysis of the promoter region of the housekeeping gene DmRP140 by sequence com A,Reference number: PQ0154; MUID:91276237; PMID:1908256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGIGADLITIFKDLNLKFAYQGKIG 216
       148 LAHVKLSNN-----TIPVGFGINETLSASKNNFAWGAGIGAKY----AVTDNIMID 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 -INGTNSLTK--KVFGLKKDGDITKKDDFTRVAPGIDFQNNLISGF----SGSIGYSMDG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 PRIELEAAYQQFNPKNTDNNDTD-----NGEYYKHFALSRKDAMEDQQYVVLKNDGITFM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 RCFVGEYYPVDVNRISALTYASFVPKMDVIYKASATETGSTDFIIDSSVNIRPIYNGAYK 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                               hemolysin A precursor - Vibrio cholerae (strain El Tor 017)
NiAlternate names: El Tor hemolysin
C.Species: Vibrio cholerae
C.Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 10-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 VFNASNNKAQILKTFPV----DNINEK-----FERKEVSGFELGVTGGVEVSGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 VGSRTNDNK------EGFYIS-----AKYNPSISHFRKFSAEETP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: hlyA
C;Superfamily: Vibrio hemolysin A
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-738/Product: hemolysin A #status predicted <MAT>
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Best Local Similarity 21.5%; Pred. No. 1.6;
Matches 63; Conservative 37; Mismatches
                                                                                                                                                         195 ASYKYINAGKVSISKNHYAGD 215
                                                                              255 A--POTTSASVTLDVGYFGGE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 SLMVNTCYDITAEGVSFVPYA-
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C;Genetics:
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Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                          14;
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C;Genetics:
A;Gene: STY0351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 TNSLTKKVFGLKKDGDITKKDDFTRVAPGIDFQNNLISGFSGSIGYSMD-----GPRI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELE-AAYQQFNPKNTDNNDTDNGEYYKHFALSRKDAMEDQQYVVLKNDGITFMSLMVNTC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 NGEYYKHFALSRKD--AMEDQQYVVLKNDGITFMSLMVNTCYDITAEGVSFVPYACAGIG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 YDFRNDS-AFTPWVSAGIG----YAKEIHQKTTGISTWDYGYGSSGRESLSRSGSADNF 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 KKDDFTRVAPGIDFQNNLISGFSGSIGYSMDGP----RIELEAAYQQFNPKNTDNNDTD 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
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A;Residues: 15-264 <RE2>
A;Cross-references: EMBL:U07174; NID:g463910; PIDN:AAC13752.1; PID:g463912
A;Accession: 169134
A;Status: translated from GB/EMBL/DDBJ
A;Andlecule type: DNA
A;Molecule type: DNA
A;Residues: 18-264 <RE3>
A;Cross-references: EMBL:U07174; NID:g463910; PIDN:AAC13753.1; PID:g463913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KILVRSALISLMSILPYQSFADPVGSRTNDNKEGFYISAKYNPSISHFRKFSAEETPING
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                                                                                                                                                                                                                                                                                                                   DB 2; Length 264;
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                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                      199
                                                                                                                                                                                                                                                                                                               8.2%; Score 119.5; DB 23.0%; Pred. No. 0.025; tive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: |: |:| :1
204 AWSLGAGVRYDVTPDIA 220
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                                                                                                                                                                                                                                                                                                                                                   Local Similarity 23.0% tes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NGEETSKY----KGGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-239 < PAR>
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